

RAW SEQUENCE LISTING

**The Biotechnology Systems Branch of the Scientific and Technical
Information Center (STIC) no errors detected.**

Application Serial Number: 10/811,080

Source: _____

Date Processed by STIC: _____

ENTERED



IFWO

RAW SEQUENCE LISTING

DATE: 10/18/2004

PATENT APPLICATION: US/10/811,080

TIME: 10:03:39

Input Set : N:\Cr3\RULE60\10811080.raw.txt

Output Set: N:\CRF4\10182004\J811080.raw

```

1 <110> APPLICANT: Gerritsen, Mary E.
2   Goddard, Audrey
3   Grimaldi, J. Christopher
4   Mehraban, Fuad
5 <120> TITLE OF INVENTION: NOVEL POLYPEPTIDES, THEIR NUCLEIC ACIDS, AND METHODS
6   FOR THEIR USE IN ANGIOGENESIS AND VASCULARIZATION
7 <130> FILE REFERENCE: P1776R2US
8 <140> CURRENT APPLICATION NUMBER: US/10/811,080
9 <141> CURRENT FILING DATE: 2004-03-26
10 <150> PRIOR APPLICATION NUMBER: US/09/684,458
11 <151> PRIOR FILING DATE: 2000-10-05
12 <150> PRIOR APPLICATION NUMBER: US 60/158,587
13 <151> PRIOR FILING DATE: 1999-10-07
14 <150> PRIOR APPLICATION NUMBER: US 60/162,611
15 <151> PRIOR FILING DATE: 1999-10-28
16 <160> NUMBER OF SEQ ID NOS: 29
18 <210> SEQ ID NO: 1
19 <211> LENGTH: 2891
20 <212> TYPE: DNA
21 <213> ORGANISM: Homo sapiens
22 <400> SEQUENCE: 1
23   ggcgaggagtc ggcgcctcgg gttcctacct cgcgtcccta ggcggcggcg 50
24   gccgggcgctc ccggg   atg gcc ttc atg gag aag ccg cca 89
25   Met Ala Phe Met Glu Lys Pro Pro
26   1 5
27   gcc ggc aag gtg ctg ctg gac gac acg gtg ccg ctg aca 128
28   Ala Gly Lys Val Leu Leu Asp Asp Thr Val Pro Leu Thr
29   10 15 20
30   gca gcc atc gag gcg agc cag agc ctg cag tcc cac acg 167
31   Ala Ala Ile Glu Ala Ser Gln Ser Leu Gln Ser His Thr
32   25 30
33   gaa tat att att cga gtg caa aga gga att tct gtg gaa 206
34   Glu Tyr Ile Ile Arg Val Gln Arg Gly Ile Ser Val Glu
35   35 40 45
36   aac agc tgg cag att gtt aga aga tac agt gac ttt gat 245
37   Asn Ser Trp Gln Ile Val Arg Arg Tyr Ser Asp Phe Asp
38   50 55 60
39   ttg ctt aac aac agc tta cag att gca ggc cta agt cta 284
40   Leu Leu Asn Asn Ser Leu Gln Ile Ala Gly Leu Ser Leu
41   65 70
42   cct ctt cct ccc aaa aaa ttg att ggt aac atg gat cgt 323
43   Pro Leu Pro Pro Lys Lys Leu Ile Gly Asn Met Asp Arg
44   75 80 85

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45   gaa ttc ata gct gaa agg cag aaa ggt ctt cag aac tat 362
46   Glu Phe Ile Ala Glu Arg Gln Lys Gly Leu Gln Asn Tyr
47           90                      95
48   ctc aac gtg atc aca aca aat cat atc ttg tct aat tgt 401
49   Leu Asn Val Ile Thr Thr Asn His Ile Leu Ser Asn Cys
50   100                      105                      110
51   gag ctg gtt aag aag ttt tta gat cca aac aac tat tcc 440
52   Glu Leu Val Lys Lys Phe Leu Asp Pro Asn Asn Tyr Ser
53           115                      120                      125
54   gca aac tat act gag att gcc ttg caa cag gtt tcc atg 479
55   Ala Asn Tyr Thr Glu Ile Ala Leu Gln Gln Val Ser Met
56           130                      135
57   ttc ttc cga tca gaa cca aag tgg gag gtg gtg gaa cct 518
58   Phe Phe Arg Ser Glu Pro Lys Trp Glu Val Val Glu Pro
59   140                      145                      150
60   ttg aaa gac ata ggt tgg aga ata agg aag aaa tat ttc 557
61   Leu Lys Asp Ile Gly Trp Arg Ile Arg Lys Lys Tyr Phe
62           155                      160
63   ttg atg aag att aaa aat cag cca aag gaa cgg cta gtg 596
64   Leu Met Lys Ile Lys Asn Gln Pro Lys Glu Arg Leu Val
65   165                      170                      175
66   tta agc tgg gct gac ctt ggc cca gac aag tat ttg tca 635
67   Leu Ser Trp Ala Asp Leu Gly Pro Asp Lys Tyr Leu Ser
68           180                      185                      190
69   gat aaa gat ttt cag tgt cta atc aaa ctt ctg cct tct 674
70   Asp Lys Asp Phe Gln Cys Leu Ile Lys Leu Leu Pro Ser
71           195                      200
72   tgt ttg cac cct tac atc tat cgg gtt acc ttt gcc aca 713
73   Cys Leu His Pro Tyr Ile Tyr Arg Val Thr Phe Ala Thr
74   205                      210                      215
75   gct aat gaa tcc tca gcg ttg cta att agg atg ttt aac 752
76   Ala Asn Glu Ser Ser Ala Leu Leu Ile Arg Met Phe Asn
77           220                      225
78   gaa aag gga aca ttg aag gat ctg atc tac aag gca aaa 791
79   Glu Lys Gly Thr Leu Lys Asp Leu Ile Tyr Lys Ala Lys
80   230                      235                      240
81   cca aaa gac cca ttt cta aag aag tac tgc aac cct aag 830
82   Pro Lys Asp Pro Phe Leu Lys Lys Tyr Cys Asn Pro Lys
83           245                      250                      255
84   aag att cag ggc ctg gaa ctc cag caa ata aaa aca tat 869
85   Lys Ile Gln Gly Leu Glu Leu Gln Gln Ile Lys Thr Tyr
86           260                      265
87   gga cgg caa ata tta gag gta ctg aag ttt ctt cat gac 908
88   Gly Arg Gln Ile Leu Glu Val Leu Lys Phe Leu His Asp
89   270                      275                      280
90   aag gga ttc cct tat ggg cat ctt cac gcc tcc aat gtg 947
91   Lys Gly Phe Pro Tyr Gly His Leu His Ala Ser Asn Val
92           285                      290
93   atg ctc gat ggg gac act tgt cgg ctg ctg gac ctt gag 986

```

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```

94 Met Leu Asp Gly Asp Thr Cys Arg Leu Leu Asp Leu Glu
95 295 300 305
96 aat tcc tta ttg ggc ctg cct tcc ttc tac cga tct tat 1025
97 Asn Ser Leu Leu Gly Leu Pro Ser Phe Tyr Arg Ser Tyr
98 310 315 320
99 ttt tca caa ttc agg aaa atc aat aca ttg gaa agt gtg 1064
100 Phe Ser Gln Phe Arg Lys Ile Asn Thr Leu Glu Ser Val
101 325 330
102 gat gtc cac tgc ttt ggc cac tta ctg tat gaa atg act 1103
103 Asp Val His Cys Phe Gly His Leu Leu Tyr Glu Met Thr
104 335 340 345
105 tat gga cga ccg cca gac tcg gtg cct gtg gac tcc ttc 1142
106 Tyr Gly Arg Pro Pro Asp Ser Val Pro Val Asp Ser Phe
107 350 355
108 cct cct gcc ccg tcc atg gct gtg gtg gcc gtg ttg gag 1181
109 Pro Pro Ala Pro Ser Met Ala Val Val Ala Val Leu Glu
110 360 370
111 tct acg ctg tct tgt gaa gcc tgt aaa aat ggc atg cct 1220
112 Ser Thr Leu Ser Cys Glu Ala Cys Lys Asn Gly Met Pro
113 375 380 385
114 acc atc tcc cgg ctg tta cag atg cca tta ttc agc gat 1259
115 Thr Ile Ser Arg Leu Leu Gln Met Pro Leu Phe Ser Asp
116 390 395
117 gtt tta cta acc act tct gaa aaa cca cag ttt aag atc 1298
118 Val Leu Leu Thr Thr Ser Glu Lys Pro Gln Phe Lys Ile
119 400 405 410
120 cct aca aag tta aaa gag gca ttg aga att gcc aaa gaa 1337
121 Pro Thr Lys Leu Lys Glu Ala Leu Arg Ile Ala Lys Glu
122 415 420
123 tgt ata gag aag aga cta att gag gaa cag aaa cag att 1376
124 Cys Ile Glu Lys Arg Leu Ile Glu Glu Gln Lys Gln Ile
125 425 430 435
126 cac cag cat cga aga ctg aca aga gct cag tcc cac cat 1415
127 His Gln His Arg Arg Leu Thr Arg Ala Gln Ser His His
128 440 445 450
129 gga tct gag gag gaa aga aaa aaa aga aag att tta gct 1454
130 Gly Ser Glu Glu Glu Arg Lys Lys Arg Lys Ile Leu Ala
131 455 460
132 cga aag aag tca aaa cga tct gct ctt gaa aat agt gaa 1493
133 Arg Lys Lys Ser Lys Arg Ser Ala Leu Glu Asn Ser Glu
134 465 470 475
135 gag cat tca gcg agg tac agc aac tcc aat aat tca gga 1532
136 Glu His Ser Ala Arg Tyr Ser Asn Ser Asn Asn Ser Gly
137 480 485
138 tct ggg gcc agc tca cct ctg acg tcc ccg tca tcg cca 1571
139 Ser Gly Ala Ser Ser Pro Leu Thr Ser Pro Ser Ser Pro
140 490 495 500
141 act cca ccc tct aca tca ggg ata tct gca tta cct cca 1610
142 Thr Pro Pro Ser Thr Ser Gly Ile Ser Ala Leu Pro Pro

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143          505          510          515
144 cct cct cca cct cca cca cca cca gca gct ccc ttg cct 1649
145 Pro Pro Pro Pro Pro Pro Pro Pro Ala Ala Pro Leu Pro
146          520          525
147 cct gcg agc acc gag gta cct gcc cag ctc tcg tct cag 1688
148 Pro Ala Ser Thr Glu Val Pro Ala Gln Leu Ser Ser Gln
149          530          535          540
150 gct gtg aat ggc atg agc cga ggg gcc ttg ctc agc tcc 1727
151 Ala Val Asn Gly Met Ser Arg Gly Ala Leu Leu Ser Ser
152          545          550
153 atc cag aat ttc caa aaa gga act ttg agg aaa gcc aaa 1766
154 Ile Gln Asn Phe Gln Lys Gly Thr Leu Arg Lys Ala Lys
155          555          560          565
156 acc tgt gat cac agt gct ccg aag atc ggc tg aa 1800
157 Thr Cys Asp His Ser Ala Pro Lys Ile Gly
158          570          575          577
159 gcttctgtt tacacttggg gggaaaagtt cttttttatt cctactcacc 1850
160 cctaccccc aaactaccct cttcctggga aagtaattgc tgagccagta 1900
161 cagccacaaa cagtactatt ttgcagatgc tcatgtaagc agcttttcga 1950
162 gagaaataat tctttaagca gaataaagtt aggctggcat tgctccctta 2000
163 agatcttgct cctttattaa ccctgtaaag gagtcttggt tctcctctaa 2050
164 tggccaggct tttgggacag cagcatattg aaatattttc accaactaaa 2100
165 ggaaatagac agaaaaacaa tgacaatatt caatcacagc agtaaattggc 2150
166 ctttgtgttg caatcccttc taccctcatca gacagctcct agaaacattc 2200
167 cttacagttc atttctctaa agcattttct gattcttaga taactccaat 2250
168 ttttgctacc tttatcttag acattaacac tatagcccaa agcatagtta 2300
169 ctttgctaaa tcagaaagca actgagttct ttgttttctc ctcaaataga 2350
170 atggggaacg ttcacaacat tctcttaagt tctaacagga ataccattgt 2400
171 gggtatagaa ctgaggctg cttaaagcaac tactctagac ccatagttct 2450
172 ttttagttag atgtattgaa acagacaaaa atattaacat cagaaaaagc 2500
173 tcttgccaat tagaggatct tcttaatcct cagcaattaa gtttgggggt 2550
174 tgaggggggc aggtcattgt tacaacagaa gttaaatttg catctataga 2600
175 aatcaattat gatttttgaa agatttatct aaatatatca atatagcatc 2650
176 tctttaatgt tagtcattta ttagaaagat cctttatcct gatttgctta 2700
177 aacctttcaa taaattgcac tttaaaggat tataaataat ccatttaaaa 2750
178 attcaagtac acacatcagt gttggttact atgcagagaa tgtcattgtg 2800
179 tatagtttca tgtaatctgt tatgtcagct gtatttttta ttaaaatcat 2850
180 gtcaagaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa a 2891
182 <210> SEQ ID NO: 2
183 <211> LENGTH: 577
184 <212> TYPE: PRT
185 <213> ORGANISM: Homo sapiens
186 <400> SEQUENCE: 2
187 Met Ala Phe Met Glu Lys Pro Pro Ala Gly Lys Val Leu Leu Asp
188 1 5 10 15
189 Asp Thr Val Pro Leu Thr Ala Ala Ile Glu Ala Ser Gln Ser Leu
190 20 25 30
191 Gln Ser His Thr Tyr Ile Ile Arg Val Gln Arg Gly Ile Ser
192 35 40 45

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193	Val	Glu	Asn	Ser	Trp	Gln	Ile	Val	Arg	Arg	Tyr	Ser	Asp	Phe	Asp
194					50					55					60
195	Leu	Leu	Asn	Asn	Ser	Leu	Gln	Ile	Ala	Gly	Leu	Ser	Leu	Pro	Leu
196					65					70					75
197	Pro	Pro	Lys	Lys	Leu	Ile	Gly	Asn	Met	Asp	Arg	Glu	Phe	Ile	Ala
198					80					85					90
199	Glu	Arg	Gln	Lys	Gly	Leu	Gln	Asn	Tyr	Leu	Asn	Val	Ile	Thr	Thr
200					95					100					105
201	Asn	His	Ile	Leu	Ser	Asn	Cys	Glu	Leu	Val	Lys	Lys	Phe	Leu	Asp
202					110					115					120
203	Pro	Asn	Asn	Tyr	Ser	Ala	Asn	Tyr	Thr	Glu	Ile	Ala	Leu	Gln	Gln
204					125					130					135
205	Val	Ser	Met	Phe	Phe	Arg	Ser	Glu	Pro	Lys	Trp	Glu	Val	Val	Glu
206					140					145					150
207	Pro	Leu	Lys	Asp	Ile	Gly	Trp	Arg	Ile	Arg	Lys	Lys	Tyr	Phe	Leu
208					155					160					165
209	Met	Lys	Ile	Lys	Asn	Gln	Pro	Lys	Glu	Arg	Leu	Val	Leu	Ser	Trp
210					170					175					180
211	Ala	Asp	Leu	Gly	Pro	Asp	Lys	Tyr	Leu	Ser	Asp	Lys	Asp	Phe	Gln
212					185					190					195
213	Cys	Leu	Ile	Lys	Leu	Leu	Pro	Ser	Cys	Leu	His	Pro	Tyr	Ile	Tyr
214					200					205					210
215	Arg	Val	Thr	Phe	Ala	Thr	Ala	Asn	Glu	Ser	Ser	Ala	Leu	Leu	Ile
216					215					220					225
217	Arg	Met	Phe	Asn	Glu	Lys	Gly	Thr	Leu	Lys	Asp	Leu	Ile	Tyr	Lys
218					230					235					240
219	Ala	Lys	Pro	Lys	Asp	Pro	Phe	Leu	Lys	Lys	Tyr	Cys	Asn	Pro	Lys
220					245					250					255
221	Lys	Ile	Gln	Gly	Leu	Glu	Leu	Gln	Gln	Ile	Lys	Thr	Tyr	Gly	Arg
222					260					265					270
223	Gln	Ile	Leu	Glu	Val	Leu	Lys	Phe	Leu	His	Asp	Lys	Gly	Phe	Pro
224					275					280					285
225	Tyr	Gly	His	Leu	His	Ala	Ser	Asn	Val	Met	Leu	Asp	Gly	Asp	Thr
226					290					295					300
227	Cys	Arg	Leu	Leu	Asp	Leu	Glu	Asn	Ser	Leu	Leu	Gly	Leu	Pro	Ser
228					305					310					315
229	Phe	Tyr	Arg	Ser	Tyr	Phe	Ser	Gln	Phe	Arg	Lys	Ile	Asn	Thr	Leu
230					320					325					330
231	Glu	Ser	Val	Asp	Val	His	Cys	Phe	Gly	His	Leu	Leu	Tyr	Glu	Met
232					335					340					345
233	Thr	Tyr	Gly	Arg	Pro	Pro	Asp	Ser	Val	Pro	Val	Asp	Ser	Phe	Pro
234					350					355					360
235	Pro	Ala	Pro	Ser	Met	Ala	Val	Val	Ala	Val	Leu	Glu	Ser	Thr	Leu
236					365					370					375
237	Ser	Cys	Glu	Ala	Cys	Lys	Asn	Gly	Met	Pro	Thr	Ile	Ser	Arg	Leu
238					380					385					390
239	Leu	Gln	Met	Pro	Leu	Phe	Ser	Asp	Val	Leu	Leu	Thr	Thr	Ser	Glu
240					395					400					405
241	Lys	Pro	Gln	Phe	Lys	Ile	Pro	Thr	Lys	Leu	Lys	Glu	Ala	Leu	Arg

RAW SEQUENCE LISTING ERROR SUMMARY
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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:5; N Pos. 162,165,183,184,187,204,207,211,216,219,222,223,225,237,240
Seq#:5; N Pos. 244,250,253,262,267,269,275,279,282,289,290
Seq#:9; N Pos. 379,433,459,492,517,541,549,561,575,579,582,710,742,774,784
Seq#:13; N Pos. 103
Seq#:13; Xaa Pos. 11
Seq#:15; N Pos. 74,1306
Seq#:16; Xaa Pos. 104
Seq#:17; N Pos. 4,107,109,112,119,122,176,323,1616,1878,1881,1911,1924,1939
Seq#:17; N Pos. 1953,1982,1991,1992,2000,2443
Seq#:17; Xaa Pos. 18,449
Seq#:18; Xaa Pos. 18,448
Seq#:19; N Pos. 300

Invalid Line Length:

The rules require that a line not exceed 72 characters in length. This includes spaces.

Seq#:9; Line(s) 511

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Input Set : N:\Crif3\RULE60\10811080.raw.txt

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L:479 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5 after pos.:150
M:341 Repeated in SeqNo=5
L:521 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9 after pos.:350
M:341 Repeated in SeqNo=9
L:565 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:13 after pos.:91
M:341 Repeated in SeqNo=13
L:830 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:15 after pos.:50
M:341 Repeated in SeqNo=15
L:938 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:16 after pos.:90
L:982 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:17 after pos.:0
M:341 Repeated in SeqNo=17
L:1144 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:18 after pos.:15
M:341 Repeated in SeqNo=18
L:1225 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:19 after pos.:250